

[NCBI](#)[Entrez](#)[BLAST 2 sequences](#)[BLAST](#)[Example](#)[Help](#)

## BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using **BLAST** engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#)

**Reference:** Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program  Matrix

Parameters used in **BLASTN** program only:

Reward for a match:  Penalty for a mismatch:

☐ Use Mega BLAST Strand option

Open gap  and extension gap  penalties

gap x\_dropoff  expect  word size  Filter ☐

Sequence 1 Enter accession or GI  or download from file  
or sequence in FASTA format from:  to:

HTHQDFQPVHLHLVALNTPLS

Sequence 2 Enter accession or GI  or download from file  
or sequence in FASTA format from:  to:

ISSANYEKPALHLAALNMPFSGDIRADFQCFKQARAAGLLSTYRAFLSSHLDL  
STIVRKAERYSLPIVNLKGQVLFNNWDSIFSGHGGQFNMHIPIYSFDGRDIMTD  
PSWPQKVIWHGSSPHGVRLVDNYCEAWRTADTAVTGLASPLSTGKILDQKAYSC  
ANRLIVLCIENSFMTDARK

Comments and suggestions to: [blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)

Credits to: [Tatiana Tatusov](#) and [Tom Madden](#)





## Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.1 [Aug-1-2001]

Matrix BLOSUM62 ☐ gap open: 11 gap extension: 1  
x\_dropoff: 50 expect: 10.0 wordsize: 3 Filter ☐ Align

Sequence 1 lc|seq\_1 Length 20

Sequence 2 lc|seq\_2 Length 181

No significant similarity was found

